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AF301018 1251 bp mRNA linear ROD 25-NOV-2000 Mus musculus strain C57BL/6 chemokine receptor CXCR6 mRNA, complete
                                                                                                                                                                  E28986 Seven-pass
B28897 Seven-pass
AC107545 Rattus no
U73314 Human G pro
BC033584 Homo sapi
AR049107 Sequence
AX549062 Sequence
AX549062 Sequence
AX3248 Homo sapien
U73529 Human G pro
AC09782 Homo sapien
AF124380 Macaca mu
AF231559 Cerrocebu
AF291671 Macaca ne
AR158353 Sequence
AR007859 Cercopith
AR188352 Sequence
AR007859 Cercopith
AR188352 Sequence
AR007859 Cercopith
AR188454 Homo sapience
AF007545 Homo sapience
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Mus musculus

Eukaryotsi Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1251)

Matloubian, M., David, A., Engel, S., Ryan, J.E. and Cyster, J.G.

A transmembrane CXC chemokine is a ligand for HIV-coreceptor Bonzo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AR366325 Sequence
AX454125 Sequence
U45982 Human G pro
AC005669 Homo sapi
                                                                                                                                    AF301018 Mus muscu
AF305709 Mus muscu
score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AY322543
AX244235
AX151463
AX15624
AR1554631
AF354631
BX546477
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AY242127
AJ132337
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AC107545
HSU73531
BC033584
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HSY13248
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AC099782
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AF354631
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Sequence

Homo sapi Homo sapi Pan trogl Homo sapi Sequence Sequence

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AF305709 1823 bp mRNA linear ROD 10-NOV-2000 Mus musculus putative chemokine receptor mRNA, complete cds. AF305709
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Mus musculus
Mus musculus
Subrayotae; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1823)
Sato, H. and Taniguchi, M.
Molecular cloning of a putative chemokine receptor preferentially expressed in mouse lymphocytes
Obbablished
TCTGGGGCCAAGTCATTTGCTTGCTCATTTGGGTGGTCTCCCTGTTGGTTTCTTTGCCAC
                                                                                                                                                             CTATGATTCTGTGCTACTCAGGCATTATCAAGACCTTGCTTCATGCTCGAAACTTCCAGA
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Sato, H. and Taniguchi, M.
Suto, H. and Taniguchi, M.
Submitted (14-SEP-2000) Department of Molecular Immunology,
Graduate School of Medicine, Chiba University, 1-8-1 Inohana
Chuo-ku, Chiba 260-8670, Japan
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1201 AACAAGAAAGCTTTGCTTATAGCATGTGGAGTATCATGGAGAAGCCTGAC
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/product="chemokine receptor CXCR6"
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/protuct="data142662"
/db xxef="d1:11442662"
/translation="MDDGHQESALYDGHYEGDFWLFNNSSDNSQENKRFLKFKEVFLP
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FWYLDYPCFGALGASIA/1171FPQKRFLTATCITVDRF1NVLVQFYKAFRQAKWINGQVI
CLLIWVVSLLVSLVSLPQIIYGHVQDIDKLICQYHSEEISTMVLVIQWTLGFFLPLLTWIL
YSGGIIKTLATARNFQHKSLKIIFLVVAVPLLTQFPRNLAMLIQSTSWEYTITSFK
YSGIIKTLATARNFQHKSLKIIFLVVAVPLLTQFPRNLAMLIQSTSWEYTITSFK
YSGIIKTLATARNFQHKFRXNVWKLWKDMKDIGCLSHLGVSSQWKSSEDSS
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                                                 Z (bases 1 to 1251)
Matloubian,M., David,A., Engel,S., Ryan,J.E. and Cyster,J.G.
Direct Submission
Submitted (30-AUG-2000) Microbiology and Immunology, University
California, San Francisco, 513 Parnassus Avenue, San Francisco,
94143-0414, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTGGGGCCCAAGTCATTTGCTTGCTTGCTTGGCACTCTCCTGTTGGCAC
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/note="receptor for CXCL16; similar to Homo sapiens
co-receptor Bonzo/STRL33/TYMSTR"
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
 Immunol. 1 (4), 298-304 (2000)
                                                                                                                                                                             /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                   'db_xref="taxon:10090"
                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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E28986.1 GI:13026577
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84.2%; Score 1053; D

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1053; Conservative 0; Mismatches
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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//dc xref="df.il15615" |
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99.8%; Pred. No. 0;
live 0; Mismatches
                   /db_xref="taxon:10090"
/tissue_type="spleen"
78. .1133
                                                                                        /note="BONZO-like"
strain="C57BL/6"
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Best Local Similarity 99.8
Matches 1231; Conservative
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7/c 7/c 7/c 7/c SION SION SION SION SION SION SION SION	PR HIROSHI ISHIMARU, NAOKO IEMURA, TAKEHIRO KOSHIO PC C12N15/09, C07K14/705, C07K16/28, C12N5/10, C12P21/02, G01N33/566, PC C12N15/00, PC C12N15/00 CC Strandedness: Single; CC Topology: Linear; FH Key Location/Qualifiers PT Source /organism='Unidentified'. UNES 11053 1.1053 1.1053 Mol_type="genonic DNA" Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Above Abov	Y Match Local Similarity 100.0%; Pred. No. 0; Local Similarity 100.0%; Pred. No. 0; hes 1053; Conservative 0; Mismatches 0; Indels 0; Gaps 78 ATGGATGATGAGCATCAAGAGTCAGCTCTGTACGATGGGCACTACGAGGAGATTTCTGG 1053 ATGGATGATGAGCATCAAGAGTCAGCTCTGTACGATGGGCACTACGAGGAGATTTCTGG 118 CTCTTCAACAATTCCAGTGATAACAGCCAGGAGAACACACTCCTAAAGGTTCTGGG 138 CTCTTCAACAATTCCAGTGATAACAGCCAGGAGAACACACTCCTAAAGGTTCAAGGAG 993 CTCTTCAACAATTCCAGTGATAACAGCCAGGAGAACACACTCCTAAAGTTCAAGGAGAGAGA	198 GTCTTTTTGCCCTGTGTGTACCTGGTATGTTTGAATGCTAGGAAACTCCTG 257 933 GTCTTTTGCCCTGTGTACCTGTAGTATGTTTGTACTTTGGAATGCTAGGAAACTCCTG 257 258 GTTCTGATTATATATATATCTACCAGAAGCTGAGGACTTCTGACAGATGTTTTTGTGTT 873 GTTCTGATTATATATATATCTACCAGAAGCTGAGGACTCTGACAGATGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTG	378 ACCTATGAGTGCTTTTGGCACAGTGATGAACTCTTCGAGGCATGTATACAATG 753 ACCTATGAGTGGTCTTTGGCACAGTCATGTGCAAACTCTTCGAGGCATGTATACAATG 438 AACTTCTACGTGCTCATGGTCATCTCACCTGCATCAACTCGTTCATTGTAGTG 693 AACTTCTACGTGCTCATCGTCACCTCCACCTGCATCAATGTAGTG 694 GTCCAGGCTACCAAGGCCTTCAACTGCATCGATCGTTTCATTGTAGTG 637 GTCCAGGCTACCAAGGCCTTCAACTGCATCGATCGTATCATTGTAGTG 638 GTCCAGGCTACCAAGGCCTTCAACTGCATCGAAGATCTGGGGCCAAGTCATT 557 GTCCAGGCTACCAAGGCCTTCAACTGGCAAGTCGTT 574 GTCCAGGCTACCAAGGCCTTCAACTGGCAAGTCGTT 575 GTCCAGGCTACCAAGGCCTTCAACTGGCAAGTTCATT 576 GTCCAGGCTACCAAGGCCTTCAACTGGCAAGTCATT 577 GTCCAGGCTACCAAGGCCTTCAACTGGCAAGTCATT 577 GTCCAGGCTACCAAGTCCAACTGGCAAGTCATT 577 GTCCAGGCTACCAACTGGCAAGTCAATT 577 GTCCAGGCTACCAAGTCCAACTGGCAAGTCAATT 578 GTCCAGGCTACCAAGTCCAACTGGCAAGTCAATT 578 GTCCAGGCTACCAAGTCCAACTGGCAAGTCAATT 579 GTCCAGGCTACCAACTGCAACTGCAAGTCAATT 579 GTCCAGGCTACCAACTGCAACTGCAAGTCAATT 579 GTCCAGGCTACCAACTGCAAGTCCAATT 570 GTCCAGGCTACAATT 570 GTCCAGG
RESULT E28987/ LOCUS DEFINIT ACCESSI VEX SION KEYWORD SOURCE ORGAN REFEREN TITLE JOURN	, FEATURES SOU	ORIGIN Ouer Best Matc Oy Db	8 6 6 6 6	6 6 6 6 6
78 ATGGATGATGAGGATCAAGAGTCAGTTACGATGGGCACTACGAGGAGATTTCTGG 137	ACCTATGAGTGGGTCTTTGGCACAGTCATGTGCAAAACTCTTCGAGGCATGTATACAATG ACCTATGAGTGGGTCTTTGGCACAGTCATGTGCAAAACTCTTCGAGGCATGTATACAATG ACCTATGAGTGCTCTTTGGCACATCATGTGCAAACTCTTCGAGGCATGTATACAATG AACTTCTACGTGTCCATGCTCACTCTCACTGCATCAGTGGATCGTTTCATTGTAGTG AACTTCTACGTGTCCATGCTCACTCACTGCATCAGTGGATCGTTTCATTGTAGTG AACTTCTACGTGTCCATGCTCACTCACTCACTGCATCGATTGTTGTAGTG AACTTCTACAGTGTCTAACCGCACACACTCAGTGGATCGTTCATTGTAGTGTTTTTAACTGAGTCATTTTTAACTGTAACTGAGTCATTTTAACTGTAACTGAAAACTGAAAATTTTAACTATTTTAACTATTTTAACTAATTTAACTAATTTAACTAATTTAACTAATTTAACTAATTTAACTAATTTAACTAATTTAACTAATTTAACTAATTAACTAATTAACTAATTAACTAATTAACTAATTAACTAATTAACTAATTAATTAACTAATTAATTAACTAATTAATTAACTAATTAACTAATTAACTAATTAACTAATTAATTAACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATA	GGCCAT ATGGTT ATGGTT TGCTAC TGCTAC TGCTAC TGCTAC TGCTAC TGCTAC TGCTAC	798 ATCATCTTCCTTGTAGTGGCTGTTCTGCTGACCCAGACACCCTTCAACCTTGCCATG 857	978 GGCTTAAAGTTCCGGAAGACGTCTGGAAACTTATGAAGGATATCGGCTGCCTCTCTCAC 1037

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Rattus norvegicus clone CH230-150D22, WORKING DRAFT SEQUENCE, 6
unordered pieces.
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                                                     677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         918 GIGACAGAGGCIATAGCATACTITICGGGCTIGCCTTAACCCTGTACTITATGCCTTTGTT 977
                                                                                                                                                                                                                                                                                                            797
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                                                                                                                        454
                                                                                                                                                                                 CTTGTTATACAGATGACTCTGGGGTTCTTCCTGCCATTGCTCACTATGATTCTGTGCTAC 737
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                            GTTCAAGATATTGACAAGCTTATCTGTCAGTACCACAGTGAGGAGATATCCACTATGGTT
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HTG: HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Conter clone name: GZSX
Center clone name: GZSX
Contact clone name: GZSX
Assembly program: Phrap; version 0.990329
Consensus quality: 212104 bases at least Q40
Consensus quality: 222104 bases at least Q30
Consensus quality: 222280 bases at least Q30
Consensus quality: 222280 bases at least Q30
Consensus quality: 222280 bases at least Q30
Consensus quality: 722280 bases; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Attus norvegicus (Norway rat)
Rattus norvegicus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
         AGTGGTCCAGGCTACCAAGGCCTTCAACAGGCAGGCTAAGTGGAAGATCTGGGGCCCAAGT
                                                                                                                                                                                                                                                                           146342 GGTTCTTGTTCTACAGATGACTCTGGGGTTCTTCCTGCCATTGCTCACTATGATTCTGTG
                                                                                                   146222 cacingcingcicalcidegiagiciccingcingcinicinisceaeagaicalcae
                                                                                                                                                                              146282 CAGAGTIGGACATATIGACAGGCTTATCIGICAGTICCACAAGGCGATATCGACGT
                                                         CATTIGCTIGCTCATTIGGGIGGICICCCIGITIGGITICITIGCCACAGAICATCIAIGG
                                                                                                                                                   CCATGITCAAGAIATIGACAAGCITATCTGTCAGTACCACAGTGAGGAGATATCCACTAT
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NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in his sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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8803 212162: gap of unknown length
8812 215820: contig of 3658 bp in length
8821 21520: gap of unknown length
8821 229332: contig of 13412 bp in length
8822 229432: gap of unknown length
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8859 231958: gap of unknown length
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8859 231959: contig of 1001 bp in length.
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/note="clone_boundary

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Direct Submission

Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:23608101.

The sequence in this assembly is a combination of BAC based reads and whole genome shorgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence and sequence an
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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Direct Submission
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                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft' sequence It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                              Assembly program: Atlas 3.0;
Consensus quality: 227338 bases at least Q40
Consensus quality: 23169 bases at least Q30
Consensus quality: 23164 bases at least Q20
Estimated insert size: 237900; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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18430: gap of unknown length
251789: contig of 233359 bp in length
251889: gap of unknown length
253204: contig of 1315 bp in length
253304: gap of unknown length
254420: contig of 1116 bp in length.
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Best Local Similarity 91.7%; Pred. No. 4.8e-303;
Matches 1078; Conservative 0; Mismatches 96; Indels
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Location/Qualifiers
1. .254420
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Center project Information
Center project name: GKRI
Center clone name: CH230-226016
                                                                         Summary Statistics
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Jepne="STRL33"

/note="contains allelic differences compared to STRL33.1

encoded by GenBank Accession Number U73529; contains seven

transmembrane domains"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVSLPQIIYGNVFNLDKLICGYHDBAISTVVLATQMTLĞFFLPLLTMIVCYSVIIKTL
LHAGGFQKHRSLKIIFLVMAVFLLTQNPPNLMKFIRGTHWBYYAMTSFHYTIMVTBAI
AYLRACLNPVLYAFVSLKFRKNFWKLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNV
BATGMFQL"
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9166430

2 (bases 1 to 2804)

Liao,F and Farber,J.M.

Direct Submission.

Submitted (07-021-1996) Laboratory of Clinical Investigation,

Submitted (07-021-1996) Laboratory of Clinical Investigation,

National Institute of Allergy and Infectious Diseases, NIH, 9000

Rockville Pike, Bldg 10, Rm 11N-228, Bethesda, MD 20892, USA

Location/Qualifiers
 STRL33, A novel chemokine receptor-like protein, functions as a fusion cofactor for both macrophage-tropic and T cell line-tropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCAACAATTCCAGTGATAACAGCC---AGGAGAACAAACGCTTCCTAAAGTTCAAGGAG
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                                                    J. Exp. Med. 185 (11), 2015-2023 (1997) 97311099
                                                                                                                                                                                                                                                                                                                      'note="expressed in T cells"
                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                         1. .2804
/gene="STRL33"
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Human G protein-coupled receptor STRL33.3 (STRL33) mRNA, complete
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Liao,F., Alkhatib,G., Peden,K.W., Sharma,G., Berger,E.A. and Farber,J.M.
                                                                                                         AGTGGTCCAGGCTACCAAGGCCTTCAACAGGCAGGCTAAGTGGAAGATCTGGGGCCAAGT
                                                                                                                                                                                                                                                        AATGAACTTCTACGTGCCATGCTCACTCTCACCTGCATCACAGTGGATCGTTTGTTGT
                                         AATGAACTTCTACGTGTCCATGCTCACCTCACCTGCATCACGTGGATCGTTGT
                                                                                    AGTGGTCCAGGCTACCAAGGCCTTCAACCGGCAGGCTAAGTGGAAGATCTGGGGCCAAGT
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VERSION
KEYWORDS
SOURCE
ORGANISM
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Contact: MgC help desk.
Email: gapbs r@mail.nih.gov
Email: gapbs r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., M., Bo.S.-L., Karline, E., Kwong, P., Legaspi, R.,
Maduro, Q.L., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
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/protein id="AAH33584.1"
/brotein id="AAH33584.1"
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/db_xref="Locus1D:10663"
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SELGATYTINFYTSMLILICTIVUDETFVVVKATXAYNQQAKRHTWGKVTSLLIWVISL
IVVSLPQIIYQRVFNLDJKLICGYHDBALSTVVLATYATNQTGFELPLLIMIVVCSVIIKTL
LHAGGFQKHRSLKIIFLVMAVFLLTQMPFNLMKFIRSTHWBYYAMTSFHYTIMVTBAI
AYRACLINVLYAFVSLKFRKNFWKLVKDIGCLPVLGVSBDNSKTFSSASHNV
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/note="7tm_1; Region: 7 transmembrane receptor (rhodopsin
family)"
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5730105.
Location/Qualifiers
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Schein, J.E., Jones, S.J. and Marra, M.A. human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/note="synonyms: STRL33,
/db_xref="LocusID:10663"
/db_xref="MIM:605163"
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Direct Submission
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Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Edeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N. K.,
Hopkins, R.F., Jordan, H., Morce, T., Wans, S.I., Wang, J., Hsich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Rtchards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 1923)

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us-10-603-141-1.rge

PAT 29-SEP-1999

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CACAATGTGGAGGCCACCAGCATGTTCCA - - GTTATAGGCCTTGCCAGGGTTTCGAGAA 1082
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                                                                                                                                                                                                                                                                                                         Ellis, C.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2238
                                                                                                                                                                                                                                                                                            1 (bases 1 to 2238)
Bishourbagy, N.B., Bergsma, D.J.P.O.Box.1.5.3.9. and Human 7-transmembrane receptor and DNA
Patent: US 5824504-A 1 20-OCT-1998;
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/organism="unknown"
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                                                                                  TTATAGCATGTGGAGTATCATGGAGAAG 1245
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AR049107
AR049107.1 GI:6005146
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Best Local Similarity 78.6
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                               TTAATAACAGAATTCTAGGAGCATGGTGTATCATTTGGATGCAACAAGAAAGCTTTGC
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Patent: WO 02061087-A 347 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
Location/Qualifiers
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Pred. No. 2.4e-208;
0; Mismatches 232;
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 78.5%;
Matches 870; Conservative (
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                                 GTTAAGGCCACCAAGGCCTACAACCAGCAAGCCAAGAGGATGACCTGGGGCAAGGTCACC
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GLVGNSLVLVISIFYHKLQSLTDVFLVNLPLADLVFVCTLPFWAXAGIHEWVFGQVMC
KSLLGTYTNIPTSMLILTCITVDRFTVVKAATANQOGAKAWWGKVTSLLWTSL
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AYLRACLNPVLYAFVSLKFRKNFWKLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNV
                                                                                                                                                                                                                                                                            Loetscher, M., Amara, A., Oberlin, E., Brass, N., Legler, D.F.,
Loetscher, P., D'Apuzzo, M., Meese, E.U., Rousset, D., Virelizier, J.L.,
Baggiolini, M., Arenzana-Seisdeos, F. and Moser, B.
TYMSTR, a puteative chemokine receptor selectively expressed in
activated T cells, exhibits HIV-1 coreceptor function
Unpublished
2 (bases 1 to 1953)
Loetscher, M.
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Catarrhini; Hominidae; Homo.
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Direct Submitted (19-MAY-1997) M. Loetscher, Theodor-Kocher Institute,
Submitted (19-MAY-1997) M. Loetscher, Theodor-Kocher Institute,
University of Bern, Freiestrasse 1, CH-3012 Bern, SWITZERLAND
Location/Qualifiers
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/product="orphan chemokine receptor"
/protein_id="CAA73698.1"
/db_xref="GI:2370180"
/db_xref="GOA:0016574"
/db_xref="SMISS-PROT:000574"
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/cell_type="T lymphocytes"
/tissue_type="blood"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="3"
                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                      Homo sapiens mRNA for orphan v13248
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1 (Dases 1 to 20972)

Kaul, R. K., Olson, M. V., Zhou, Y., James, R. A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K. A., Raymond, C. and Haugen, E. D.
            TGCTTGCTCATTTGGGTGGTCTCCCTGTTGGTTTTTTGCCACAGATCATCTATGGCCAT
                                                                                                                                                                     CTTGTTATACAGATGACTCTGGGGTTCTTCCTGCCATTGCTCACTATGATTCTGTGCTAC
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AC099782.2 GI:20270170
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Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
Submitted (21-NOV-2001) Genome Center, University of Washingt
Box 352145, Seattle, WA 98195, USA
3 (bases I to 20972)
3 (bases I to 20972)
5 Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.
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AYLRAGFQCATCHONDATAFVSLKFRKNFWKLVKDIGCLPYLGVSHQWKSSEDNSKTFSASHNV

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Lidao,F. and Ratber,J.M.
Direct Submission
Submission
Submitted (07-0CT-1996) Laboratory of Clinical Investigation,
National Institute of Allergy and Infectious Diseases, NIH, 9000
Rockville Pike, Bldg 10, Rm 11N-228, Bethesda, MD 20892, USA
Location/Qualifiers
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/note="expressed in tumor infiltrating lymphocytes"
1 (bases 1 to 1918)
Liao,F., Alkhatib,G., Peden,K.W., Sharma,G., Berger,E.A.
Farber,J.M.
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/note="contains seven transmembrane domains"
                                                         STRI33, A novel chemokine receptor-like protein fusion cofactor for both macrophage-tropic and
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/db_xref="taxon:9606"
/chromosome="3"
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oct Submission iitted (23-APR-2002) Genome Center, University of Washington, 352145, Seattle, WA 98195, USA yr 23, 2002 this sequence version replaced gi:17027297. Center: Genome Center Center: University of Washington Genome Center Web site: http://www.ashington.edu Contact: uwgchcgs@u.washington.edu Drafting Center: BCM Drafting Center: BCM Center project Information Center project Information Center project name: chora.	Center close name: RP11-852E15 (bc0572)	nlit m. qua sss risi	This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. Sequence Validation: This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The sequence has been validated by multiple Complete Digest fragments with sequence-predicted fragments is given below. The electronically digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines. EDORI SeqDermap Figerrat SeqDermap Figerrate SeqDermap Figerrat SeqDermap Figerrate	15519 16344 2966 2960 2067 2076 6486 963 9576 512 <800 1858 1823 449 <800

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                                                                                                                                                                                                                                                                                                                                                                                                                             6; Gaps
                                                                                                                                                                                                                                                                                                                                     Length 219553;
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                56.3%; Score 704.8; DB 2; 78.5%; Pred. No. 6.6e-208; ive 0; Mismatches 232;
/mol_type="genomic DNA"
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/chromosome="3"
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                                                                                                                                                   /map="3p21.3"
/clone="RP6-153f14"
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 78.5
Matches 870; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     678 (
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GCTTCCTAAAGTTCAAGGAGGTCTTTTTGCCCTGTGTACCTGGTAGTGTTTGTCTTTG

178

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CTTGGGGTCTCACATCAATGGAAATCTTCTGAGGACAATTCCAAGACTTTTTCTGCCTCC 46807
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/db_xref="G1:487755"
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/db
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Macaca mulatta chemokine receptor bonzo (STRL33) gene, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
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(Dases 1 to 1032)
Margulies, B. J., Hauer, D. A. and Clements, J. E.

Identification and comparison of eleven rhesus macaque chemokine
                                                                                                              CACAATGTGGAGGCCACCAGCATGTTCCA---GTTATAGGCCTTGCCAGGGTTTCGAGAA
                                                                                                                                                                                                    TTAATAACAGAATTCTAGGAGCATGGCTGTATCATTTGGATGCAACAAGAAAAGCTTTGC
                                                                   CACAATGTAGAGACCACCAGTATGTTCCAATTGTAGTAGGCCTTGCCACACTTAGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 1032)
Margulies B.J., Hauer, D.A. and Clements, J.E.
Direct Submission
Submitted (27-JAV-1999) Comp. Med., Johns Hopkins University,
Rutland Ave., Baltimore, MD 21205, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 1.9e-205;
0; Mismatches 190; Indels
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    .>1032
    gene="STRL33"
    product="chemokine receptor bonzo"

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'product="chemokine receptor bonzo"
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    1032
/organism="Macaca mulatta"
/mol_type="genomic DNA"
/db_xref="taxon:9544"

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Macaca mulatta
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Best Local Similarity
Matches 823; Conserv
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KEYWORDS
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AF124380
LOCUS
DEFINITION
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AUTHORS
TITLE
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ACGAGGGAGATTTCTGGCTCTTCAACAATTCCAGTGATAACAGCC---AGGAGAACAAAC 177

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ACTATGAAGATGATGGGTTCCTCAACAGTTTCAATGACAGCAGCAGGAGGAGCATCAAG

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TIGITGGCITAAAGITCCGGAAGAACGICTGGAAACTTAIGAAGG 1017
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                                                                                                                                                             CCTITIGGGCCTATGCAGGCACCTATGAGTGGGTCTTTGGCACAGTCATGTGCAAAACTC
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        ACTICCTGCAGTTCAGGAAGGTCTTTCTGCCCTGCATGTACCTGGTGGTGTTTGTCTGTG
                                                                 GCCTGGTGGGGAACTCCCTGGTGCTGTATCCATCTTCTACCATAAGCTGCAGAGCC
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                                    GACTGCTAGGAAACTCCCTGGTTCTATATACATTTTTCTACCAGAAGCTGAGGACTC
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Adc22542 Human G p Ab242725 Human C-C Ad323916 Homo sapi Aca56497 Human sig Abx15306 Human CC Aq66164 Human CC Aq66164 Muxine V3 Aav18351 Muxine V3 Aav31711 Muxine V3 Ab54240 Mouse 7 t Ab197940 Non-endog Ada30715 DNA encod Adc2694 Human G p Add5692 Mouse cmk Add2454 Mouse cmk Add6691 Mouse cmk Add6691 Mouse cmk Add6691 Mouse cmk Add72193 Mouse cmk Add72193 Mouse cmk Add72192 Mouse cmk Add72192 Mouse cmk Add72192 Mouse cmk Add72192 Mouse cmk Add72474 Mouse cmk Add72474 Mouse cmk Add74747 Mouse cmk Ada54274 Mouse cmk	de secuence de	okine receptor; asthma; leukocyte migration; GPCR; dulation; antyviral response; ise; G-protein coupled receptor; isl proliferation; regeneration; ceptor 941D12" gnated C may be C or T"	Gorman DM, Zlotnik A;
1074 9 ADC22542 2462 7 ABA242755 2577 6 AAD32216 2577 7 ABX15306 2751 2 AAC65164 2751 2 AAC65164 2751 2 AAC86164 2751 2 AAC81351 2751 3 AAA91711 2751 3 AAA91711 110 6 ABX54240 1107 4 AAC6050 1074 3 AAA30715 1137 8 ADC22694 1137 8 ADC22694 1137 8 ADC22694 2072 7 AAD56092 2072 7 AAD56092 2072 7 AAD56091 2072 7 AAD56091		human, rodent; chem hee; immune response; chemoattractant; mc modification respon ipid turnover; abnorm ation/Qualifiers 975 cag= a chemokine re 2 dag= b reag= cag reag= cag reag= cag reag= d	WO-US000902. US-0036715P. CORP. -Trejo H, Hedrick JA,
254 183.4 183.4 183.4 14.7 226 183.4 14.7 1833.4 14.7 229 183.4 14.7 229 183.4 14.7 33 181.2 14.5 33 181.2 14.5 33 181.2 14.5 34 177.8 14.5 35 177.8 14.5 36 177.8 14.3 37 177.8 14.3 38 177.8 14.3 39 177.8 14.3 37 177.8 14.3 38 177.8 14.3 39 177.8 14.3 39 177.8 14.3 37 177.8 14.3 38 177.8 14.3 39 177.8 14.3	1011 1 43795 AAV43795 standard AAV43795; 20-OCT-1998 (fir	XXXXX Chemokine; primate KW inflammatory respon KW inflammatory respon KW cellular morphology KW phosphoinositide li XX atrophy; 941012; ss XX XX Mus sp. Los FT CDS FT CDS FT CDS FT FT FT The FT FT Tunsure FT THE	W09832858-A2. 30-JUL-1998; 22-JAN-1997; 9 23-JAN-1997; 9 (SCHE) SCHERING MATTSON JD, SOT WPI; 1998-427954 P-PSDB; AAW70001

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                                                                                                                        This represents a rodent chemokine receptor 941D12 nucleotide sequence. The invention provides novel primate and rodent chemokines and chemokines are receptors. The chemokines, receptors and binding compounds (Optionally antibodiess/fragments specifically binding the chemokines) are useful the chemokines as sociated with abnormal physiology or development e.g. inflammatory conditions such as sathma. Chemokines are important in immune and inflammatory responses in that they induce lewiportant in immune and inflammatory responses in that they induce lewiportant in immune and inflammatory responses in that they induce lewiportant in immune and inflammatory responses in that they induce several cells involved in inflammation and can induce other biological responses e.g. modulation of second messenger levels (e.g. Ca++).

CC cellular morphology modification responses, phosphoinositide lipid turnover, possible antiviral responses etc. The chemokine receptors of turnover, possible antiviral responses, phosphoinositide lipid turnover, possible antiviral responses to The chemokine receptor polypeptides are useful to produce involve chemical antagonists which block complex production or utilise competitive binding. Binding compounds identified (agonists or network macrophages or lymphocytes) to treat e.g. abnormal produce antabodies useful diagnostically, for drug screening produce probes for detecting the polyputcleotides are useful to produce antabodies useful diagnostically from other species. They also allow transformation of cells for polypeptide production
Rodent and primate chemokines and chemokine receptors - useful diagnostically and therapeutically to treat conditions associated with abnormal physiology or development e.g. inflammatory conditions.
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                                                                                      Example 3; Page 97-99; 105pp; English.
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134 123 194 183 254 243 314 303 374 423 363 434 494 424 ATGAACTTCTACGTGTCCATGCTCACTCTCACCTCCATCACAGTGGATCGTTTCATTGTA 483 GIGGICCAGGCTACCAAGCCTICAACCGCAGGCTAAGIGGAAGAICIGGGGCCAAGIC 554 63 304 CIGAACTIGCCCCTGGCTGACCTGGTTTTGTCTGTACTCTGCCCTTTTGGGCCTATGCA GGCAGACCTTTAGTGAGCACACTTCACTCTGGAACAAGCTACTGGGCTTCTCTTCTGAT 184 GAGGTCTTTTTGCCCTGTGTGTACCTGGTAGTGTTTGTCTTTGGACTGCTAGGAAACTCC 244 credrictearrararacarrircraccadaaccreagacrergacadargrericre GGCACCTATGAGTGGTCTTTGGCACAGTCATGTGCAAAACTCTTCGAGGCATGTATACA GGCAGACCTTTAGTGAGCACACTTCACTCTGGAACAAAGCTACTGGGCTTCTCTTCTGAT GCCATGGATGATGGGCATCAAGAGTCAGCTCTGTACGATGGGCACTACGAGGGAGATTTC TGGCTCTTCAACAATTCCAGTGATAACAGCCAGGAGAACAAACGCTTCCTAAAGTTCAAG 195 GAGGICTITITGCCCTGTGTGTACCTGGTAGTGTTTGTCTTTGGACTGCTAGGAAACTCC CTGGTTCTGATTATATACATTTTCTACCAGAAGCTGAGGACTCTGACAGATGTGTTTCTG CTGAACTTGCCCCTGGCTGACCTGGTGTTTGTCTGTACTCTGCCCTTTTTGGGCCTATGCA 435 ATGAACTICTACGIGICCAIGCICACTCICCACCIGCAICACAGGGGAICGIIICAIIGIA Gaps 2 Score 1210; DB 2; Length 1475; Pred. No. 0; 0; Mismatches 5; Indels 2; Query Match Best Local Similarity 99.4%; Matches 1225; Conservative (15 4 75 64 375 (135 124 255 315 495 ò Db qq

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484 GTGGTCCAGGCTACCAAGGCCTTCAACCGGCAGGCTAAGTGGAAGATCTGGGGCCAAGTC
                                                                        544 ATTIGCTIGCTCATTIGGGIGGICTCCCTGIIGGIITICIITIGCCACAGAICAICAIGIGC
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leukocyte function, control, drug, ss.
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                    GGCTTAAAGTTCCGGAAGAACGTCTGGAAACTTATGAAGGATATCGGCTGCCTCTCTCAC
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TTAATCCAAAGTACAAGCTGGGAGTACTATACCATAACCAGCTTTAAGTATGCCATCGTA
                                                                                             GTGACAGAGGCTATAGCATACTTTCGGGCTTGCCTTAACCCTGTACTTTATGCCTTTGTT
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detecting drug controlling function of leukocyte.
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ive 0; Mismatches
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leukocyte function; control;
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P-PSDB; AAY23825.
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Human, 7-transmembrane receptor; HBMBU14; infection; HIV; cancer; asthma; anorexia; Parkinson's disease; acute heart failure; atherosclerosis; costeoporosis; angina pectoris; myocardial infarction; psychotic disorder; benign prostatic hypertrophy; neurological disorder; therapy; Huntington's disease; Gilles de la Tourette's syndrome; ds.

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This sequence encodes the human HBMBU14 protein of the invention. HBMBU14 is a human 7-transmembrane (TM) receptor. The products can be used for treating or preventing conditions related to abnormal HBMBU14 expression or activity, e.g. infections such as bacterial, fungal, protozoan and viral infections especially infections caused by HIV-1 and HIV-2, pain, cancers, anorexa's pullimia, asthma, parkinson's disease, acute heart failure, atherosclerosis, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, ulcers, asthma, allorates, including anxiety, schizophrenia, manic depression, delirium, dementia or severe mental retardation, and dyskinesias, such as Huntington's disease or Gilles de la Tourette's syndrome. The products can also be used for diagnosing a disease or susceptibility to a disease related to the expression of HBMBU14 and for identifying compounds which indice to and activate or inhibit a receptor for the polypeptide
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AAV24017 standard; cDNA;

Human HBMBU14 coding sequence.

07-AUG-1998

AAV24017;

RESULT 4
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growth-related disease, cell regeneration-related disease, AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; ALADS, march disease; and therosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease, multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;

ulcer; gene; ds

WO200261087-A2. Homo sapiens.

08-AUG-2002

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New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.

JP;

Brown

Burmer GC, Roush CL, WPI; 2003-046718/04.

P-PSDB; ABP81931.

19-DEC-2000; 2000US-0257144P. (LIFE-) LIFESPAN BIOSCIENCES

19-DEC-2001; 2001WO-US050107

Disclosure; Fig 1; 523pp; English.

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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino caids. Also described: (I) an assay for the detection of a particular of protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or anticity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR. (I) can be used as GPCRs modulators and in gene therapy. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for corresponding GPCRs. The antigenic peptides for treating immune-related diseases, immunological-related cell proliferative cipenation immune diseases, immunological-related cell proliferative diseases, or autoimmune diseases, eg. ALDS, Alzheimer's disease, atterations, allergies, Crohm's disease, practicions, allergies, Crohm's disease, practicions, allergies, Crohm's disease, giabletes, graft versue host cinflammation, allergies, cancer, cardiomyopathy, chronic and acute inflammation, allergies, moltiple sclerosis, pain, pscriasis, cancer, depression, schizophrenia, dementia, mental retardation, memory correspondersion, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis ABP22523 to ABP2269 encode GPCR proteins given in ABP81018, which are used in the exception of the present invention
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RESULT 6 AAV68515 ID AAV68515 standard; DNA; 1918 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated fusion accessory factor STRL33 - which mediates HIV infection of cells, used to develop products for the study, prevention and therapy of HIV-related disorders.
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                                                                                           STRL33; human; HIV-1; HIV related disorder; therapy; CD4; diagnosis;
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llarity 78.5%; Pred. No. 9.3e-209;
Conservative 0; Mismatches 232;
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Matches 870; Conserv
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22-JAN-1999
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Kewalramani VN;

Unutmaz D,

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This cDNA clone codes for pig-tailed macaque Bonzo (see AAW97785), a novel HIV/SIV translocation promoting agent that acts in conjunction with code to serve as a receptor for the entry into.a cell of a virus having a specific viral envelope glycoprotein. Bonzo is a member of the 7-transmembrane G-protein coupled receptor family, is closely related to transmembrane G-protein coupled receptor family, is closely related to the chemokine receptor family, and is expressed in lymphoid tissues. The invention provides the amino acid sequences (see AAW97783-88) and DNA sequences (see AAW97783-88) and DNA sequences (see AAW97783-88) and DNA sequences covel receptors were identified using an expression promoting agents. They were found to be used by particular strains of HIV-2 and retopic HIV-1. The invention also includes: mammalian cells transfected with Bonzo and/or Bob and human CD4, which can be used to Screen potential therapeutic agents and identify ligands, antibodies to Bonzo, which can be used therapeutically, e.g. as antagonists or to target to taxing or radioisotopes to HIV-permissive cells; transgenic animals; and antisense and ribozyme molecules, which may also be used therapeutically, generally antisense and ribozyme molecules, which may also be used therapeutically.
                                                                                                                                                                                          New nucleic acid encoding the human translocation promoter Bonzo - use
to screen for potential agents for treating acquired immune deficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1029 BP; 230 A; 278 C; 236 G; 285 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                       Disclosure; Page 81-82; 97pp; English.
                            98WO-US014857
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                                                                                                                   Deng H,
                                                                                                                                                WPI; 1999-132164/11.
P-PSDB; AAW97785.
                            17-JUL-1998;
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28-JAN-1999
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Score 689.4; DB 2; Length 1029;
Pred. No. 4.2e-204;
0; Mismatches 205; Indels 0;
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SIV receptor; HIV receptor; Bonzo; translocation promoting agent; G protein coupled receptor; chemokine receptor; AIDS; infection; virus transmission; pig-tailed macaque; ds.

WO9903888-A1

receptor protein Bonzo cDNA

Pig-tailed macaque HIV/SIV

(first entry)

21-MAY-1999

AAX07291;

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WPI; 2001-424455/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Pigtailed macaque cDNA encoding the SIV translocation agent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pigtailed macacque; Bonzo; simian immunodeficiency virus; SIV translocating agent; CD4; BOB; Brother of Bonzo; acquired immunodeficiency syndrome; AIDS; SIV; HIV; ss.
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The sequence encodes a novel SIV (Simian immunodeficiency virus) translocating agent, Bonzo. The invention relates to selecting an agent that may be used in treating acquired immunodeficiency syndrome (AIDS) comprises administering a potential therapeutic agent to a cell expressing human CD4 and primate Bonzo or BOB (Brother of Bonzo), contacting the cell with a virus pseudotyped with an HIV envelope glycoprotein, and measuring the cell's ability to resist infection. The method is useful for selecting or identifying an agent, which can be used in treating AIDS
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Identifying an agent for treating AIDS comprises administering a potential therapeutic agent to a cell expressing human CD4 and primate Bonzo or BOB and contacting the cell with a virus pseudotyped with an HIV envelope glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1029 BP; 230 A; 278 C; 236 G; 285 T; 0 U; 0 Other;
                                                                                                                                                                                   Example 1; Col 43-44; 41pp; English.
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Matches 811; Conservative
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CIGTACTITATGCCTITIGTIGGCTTAAAGTITCCGGAAGAACGTCTGGAAACTITATGAAGG 1017
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                             CACCCTTCAACCTCGTGAAGCTCATCCGCAGCACACTGGGAGTACTATGCCATGACCA 793
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonzo, G-protein coupled receptor, receptor, STRL33; TYMSTR, retrovirus, translation promoting agent, anti-HIV; antiviral, virucide, AIDS, antiinflammatory, immunostimulant, transgenic animal; pig-tailed macaque,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the coding sequence for pig-tailed macaque Bonzo (also named STRI33 or TYMSTR). Human Bonzo (see ABB79743) has been identified as a novel G-protein coupled receptor involved in retroviral entry into cells, acting in conjunction with CD4 as a translocation.
                                                                                                                                                                                                                                                 974 CCAAGACTTTTTCTGCCTCCCACAATGTGGAGGCCACCAGCATGTTCCAGTTATAG 1029
                                                                                                                                                                                                                                CCAAGACTIGITCIGCCTCCCACAATGIAGAGACCACCAGTATGITCCAATTGIAG 1133
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                                                                                                                                                                                                                                                                                                                                                                                                                   Pig-tailed macaque G-protein coupled receptor Bonzo cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 31; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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DENG H.
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promoting agent for SIV and also for certain strains of HIV-2 and M-tropic HIV-1. Bonzo and the closely related BOB (brocher of Bonzo) are related to the chemokine receptor family and are expressed in lymphoid tissues. Use of these new receptors following experimental infection of non-human primates with SIV strains may provide important insight into viral transmission and mechanisms of SIV- and HIV-induced AIDS. The invention provides Bonzo and BOB amino acid and DNA sequences, mammalian cells transfected with Bonzo and/or BOB and human CD4, and antibodies to Bonzo. A method of identifying other translocation promoting agents is also disclosed. Cells (or transgenic animals) that express Bonzo or BOB and contain a second of the sequence of and CD4 are used to: (a) identify therapeutic agents for treating AIDS (acquired immune deficiency syndrome), by increasing the resistance of cells to infection; (b) in filters to remove viruses with HIV envelope glycoproteins from biological fluids; (c) to identify ligands for Bonzo or BOB; (d) to identify compounds that increase the immune response to a specific pathogen or vaccine by increasing Bonzo/STRIA3 expression; and contains the seconds of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (e) to identify antiinflammatory agents that reduce Bonzo/STRL33 expression and thus inhibit recruitment of memory cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.1%; Score 689.4; DB 6; Length 1029; 79.8%; Pred. No. 4.2e-204; ative 0; Mismatches 205; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1029 BP; 230 A; 278 C; 236 G; 285 T; 0 U; 0 Other;
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Matches 811; Conservative
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This cDNA clone codes for African green monkey Bonzo (see AAM97784), a novel HIV/SIV translocation promoting agent that acts in conjunction with CD4 to serve as a receptor for the entry into a cell of a vitus having a specific viral envelope glycoprotein. Bonzo is a member of the 7-transmembrane G-protein coupled receptor family, is closely related to the chemokine receptor family, and is expressed in lymphoid tissues. The invention provides the amino acid sequences (see AAM97783-89) and DNA sequences (see AAX07289-94) of human, African green monkey and pig-tailed macaque Bonzo and Bob (brother of Bonzo) transfocation promoting agents. These novel receptors were identified using an expression cloning stategy. They were found to be used by particular strains of HIV-2 and M-1 tropic HIV-1. The invention also includes: mammalian cells transfected with Bonzo and/or Bob and human CD4, which can be used to screen contential therapeutic agents and identify ligands; antibodies to Bonzo, which can be used therapeutically, e.g. as antagonists or to target
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              854 CIGIGCICTAIGCCITIGICAGCCIGAAGTIICGAAAGAACAICIGGAAACTIGIGAAGG
CACCCTTCAACCTTGCCATGTTAATCCAAAGTACAAGCTGGGAGTACTATACCATAACCA
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to screen for potential agents for treating acquired immune deficiency
syndrome.
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toxins or radioisotopes to HIV-permissive cells; transgenic animals; and antisense and ribozyme molecules, which may also be used therapeutically, particularly expressed from a gene therapy vector
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Pred. No. 9.9e-203;
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Local Similarity 81.1%;
hes 809; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying an agent for treating AIDS comprises administering a potential therapeutic agent to a cell expressing human CD4 and primate Bonzo or BOB and contacting the cell with a virus pseudotyped with an HIV envelope glycoprotein.
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                                                                                                                                                                                                                                                           onzo; simian immunodeficiency virus; SIV translocating agent; Brother of Bonzo; acquired immunodeficiency syndrome; AIDS;
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                                                                                                                                                                                                                              Green monkey cDNA encoding the SIV translocation agent, Bonzo.
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                    CCACAATGTAGAGACCACCAGTATGTTCCAATTGTAG 1133
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Pred. No. 9.9e-203;
                                       CCACAATGTGGAGGCCACCAGCATGTTCCAGTTATAG
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1. .1029
/*tag= a
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P-PSDB; AAU04033.
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Best Local Similarity
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                                                                                                                                                                                                                                                                Monkey; Bor
CD4; BOB;
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Bonzo, G-protein coupled receptor; receptor; STRL33; TYMSTR; retrovirus; translation promoting agent; anti-HIV; antiviral; virucide; AIDS;
                                                                                                                                                African green monkey G-protein coupled receptor Bonzo cDNA
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The present sequence is the coding sequence for African green monkey
Bonzo (also named STR13 or TYMSTR). Human Bonzo (see ABB79743) has been
identified as a novel G-protein coupled receptor involved in retroviral
entry into cells, acting in conjunction with CD4 as a translocation
promoting agent for SIV and also for certain strains of HIV-2 and M-
cropic HIV-1. Bonzo and the closely related BOB (brother of Bonzo) are
related to the chemokine receptor family and experimental infection of
tissues. Use of these new receptors following experimental infection of
con-human primates with SIV strains may provide important insight into
viral transmission and mechanisms of SIV- and HIV-induced AIDS. The
invention provides Bonzo and BOB amino acid and DNA sequences, mammalian
cells transfected with Bonzo and/or BOB and human CD4, and antibodies to
long disclosed. Cells (or transgenic animals) that express Bonzo or BOB
and CD4 are used to: (a) identify therapeutic agents for treating AIDS
captized immune deficiency syndrome). Dy increasing the resistance of
cells to infection; (b) in filters to remove viruses with HIV envelope
glycoproteins from biological fluids; (c) to identify ligands for Bonzo
or BOB; (d) to identify compounds that increase the immune response to a
specific pathogen or vaccine by increase the immune response to a
specific pathogen or vaccine by increasing Bonzo/STRL33 expression; and
(e) to identify antihilalmamatory agents that reduce Bonzo/STRL33
expression; and
thus inhibit recruitment of memory cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 GGTCTTTTTGCCCTGTGTACCTGGTAGTGTTTGTCTTTGGACTGCTAGGAAACTCCCT 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid encoding the translocation promoting agent Bonzo, useful e.g. in screening for agents that inhibit infection by
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antiinflammatory; immunostimulant; transgenic animal; African green monkey; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unutmaz D, Kewalramani VN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 685; DB 6; L
Pred. No. 9.9e-203;
                                                                                                  Location/Qualifiers
1. .1029
/*tag= a
/product= "Bonzo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 29; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human immune deficiency virus.
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98US-00116498.
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81.1%;
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Best Local Similarity 81.1
Matches 809; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEWALRAMANI V N.
                                                            Cercopithecus aethiops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deng H,
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UNUTMAZ D.
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333 TAACTTCTACACATCTATGCTCATCCTCACCTGCATCACTGTGGATCGTTTCATTGTAGT
                                                                                                           GAACTTGCCCCCTGGCTGACCTGGTGTTTGTCTGTACTCTGCCCTTTTTGGGCCCTATGCAGG
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586 TGGTTTCTTTGCCACAGATCATCTATGGCCATGTTCAAGATATTGACAAGCTTATCTGTC
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                                                                                                           646 AGTACCACAGTGAGGAGATATCCACTATGGTTCTTGTTATACAGATGACTCTGGGGTTCT
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SExCkine; spleen extracted chemokine; ss
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/product= "Bonzo"
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myocardial infarction; MI; stroke; glaucoma; anxiety;
prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;
prostatic hypertrophy; gene; ss.
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Pred. No. 2e-201;
0; Mismatches 181; Indels
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Best Local Similarity 81.3
Matches 787; Conservative
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P-PSDB; ABG95153.
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Antiarteriosclerotic; cardiant; vasotropic; antinflammatory; thrombolytic; antiarrhythmic; antianginal; hypotensive; gene therapy; cardiovascular; disorder; ischaemia; aortic bending; vascular heart disease; endocarditis; atrial fibrillation; heart failure; angina; cardiomyopathy; cardiac death; gene; ds.
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CTTGCCTTAACCCTGTACTTTATGCCTTTGTTGGCTTTAAAGTTCCGGAAGAACGTCTGGA
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1, Perodin J, Rodrigue-Way
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2002US-0364529P.
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2002US-0388080P.
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2002US-0404904P.
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2002US-0408070P.
2002US-0424300P.
2002US-0424300P.
2002US-0431079P.
                                                                                                                                                                                                                                                                                                                                                standard; DNA; 1029
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23-AUG-2002;
04-SEP-2002;
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05-DEC-2002;
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                                                                                                                                       The present sequence encodes a human Bonzo polypeptide. Bonzo is a CXC chemokine receptor. The specification describes a method for identifying agents (especially antibodies) which bind to Bonzo and inhibit the binding of a ligand (especially SEXCKine (spleen extracted chemokine)) and the agents per se. The agents identified may be used for the trearment of a disorder/disease related to aberrant Bonzo expression and activity, such as inflammatory disease, cancers and/or infections (e.g.
                                                                 cancers
                                                                                                                                                                                                                                                                                                                                                                              AGGAGAACAAACGCTTCCTAAAGTTCAAGGAGGTCTTTTTGCCCTGTGTGCTTGGTAG
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                                               which bind to the CXC used to treat e.g. can
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                                                                                                                                                                                                                                                                                 Sequence 1029 BP; 229 A; 275 C; 238 G; 287 T; 0 U; 0 Other;
                                               (especially antibodies)
Bonzo, and which may be
                                                                                                                                                                                                                                                     viral, bacterial and fungal infections)
                                                                                                           1; 191pp; English
   WPI; 2001-343947/36.
P-PSDB; AAB68422.
                                              Identifying agents chemokine receptor
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The invention relates to a method for identifying a compound capable of treating a cardiovascular disorder. The present invantion identifies the differential expression of 1882, 6193, 6193, 7711, 1495, 2002, 33216, 3726, 69292, 21656, 32427, 2402, 7747, 1720, 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650, 14245, 58848, 1870, 25856, 32394, 3484, 2858, 283, 2554, 9464, 17799, 2668, 43848, 3215, 12208, 2914, 51130, 1688, 283, 2554, 9464, 17799, 2668, 43848, 3215, 12208, 2914, 51130, 16989, 21833, 2917, 59590, 15992, 2094, 2252, 3474, 9792, 15400, 1452 or disgnessing, preventing and treating cardiovascular flower user useful in diagnosing, preventing and treating cardiovascular disorders, such as attentionally activated and prevention, arcenial inflammation, vascular wall remodeling, coronary microembolism, tachycardia, bradycardia, pressure overload, aortic bending, coronary artery ligation, vascular heart disease, valvular disease, including but not limited to, valvular degeneration caused by artificial valves, atrial fibrillation, long-QT syndrome, congestive heart failure, sinus node dysfunction, angina, heart failure, sinus node dysfunction, angina, heart failure, coronary arterial fibrillation, atrial flutter, pericardial disease, including but not limited to, pericardial effusion and pericardial disease, including but not limited co. pericardial effusion and pericardial disease, including but not limited co. pericardial effusion and pericardial disease, including but not limited co. pericardial effusion and pericardial disease. cardiomyopathy, myocardial infarction, coronary artery disease, coronary artery spasm, ischaemic disease, arrhythmia, sudden cardiac death and cardiovascular developmental disorders. The methods may also be used for identifying compounds that modulate cardiovascular disorders. Sequences given in ADE31644-ADE31769 represent the genes and proteins that may be regulated by a compound of the invention.

Sequence 1029 BP; 229 A; 275 C; 238 G; 287 T; 0 U; 0 Other;

225 AGGAGAACAAACGCTTCCTAAAGTTCAAGGAGGTCTTTTTGCCCTGTGTGTACCTGGTAG 0 Score 679.2; DB 9; Length 1029; Pred. No. 6.4e-201; Indels Pred. No. 6.4e-201; 0; Mismatches 182; 54.3%; 81.2%; Conservative Similarity Ma. Local Sim 166 Query Match Matches g

285 AGGAGCATCAAGACTTCCTGCAGTTCAGCAAGGTCTTTCTGCCCTGCATGTACCTGGTGG 121 retrirencieres de de de de de la constant de la con TGTTTGTCTTTGGACTGCTAGGAAACTCCCTGGTTCTGATTATATACATTTTTCTACCAGA 122 62 226

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1065 croaddacaarrecaadacrirrircigecreecaaardrogaddecaacaacarcric 1021 885 945 841 602 TCTTGCCACTGCTCACCATGATTGTCTGCTATTCAGTCATAATCAAAACACTGCTTCATG Araccardaccacriricacraccarcardacacacacacacacacacacacaracacaca CTTGCCTTAACCCTGTACTTTATGCCTTTGTTGGCTTAAAGTTCCGGAAGAACGTCTGGA AACTTATGAAGGATATCGGCTGCCTCTCTCACCTGGGAGTCTCAAGGAATGGAAGTCTT recreaceceácarecerricaacereargaagricareceeaecaeaeaearaer ATACCATAACCAGCTTTAAGTATGCCATCGTAGTGACAGAGGCTATAGCATACTTTCGGG ccreccitaAcccretecricianecentrercaeccreaAcriteGaAAGAACTICTGGA AACTTGTGAAGGACATTGGTTGCCTCCCTTACCTTGGGGTCTCACATCAATCTT CTGAGGACAGTTCCAAGACTTGTTCTGCCTCCCACAATGTAGAGACCACCAGTATGTTCC TGCTGACCCAGACACCCTTCAACCTTGCCATGTTAATCCAAAGTACAAGCTGGGAGTACT CTCGAAACTTCCAGAAGCACAAATCTCTAAAGATCATCTTCCTTGTAGTGGCTGTGTTCC AATTGTAG 1133 AGTTATAG 1029 9001 1066 962 826 722 782 946 842 902 994 662 886 δ 임 8 8 8 6 8 Ср ò g d ò

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ALIGNMENTS

1 1 AK052901 1791 bp mRNA linear HTC 20-SEP-2003 10N Mus musculus 16 days neonate heart CDNA, RIKEN full-length enriched 11brary, clone:DB30030F09 product:chemokine (C-X-C) receptor 6, full insert sequence.	NO		RS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itch, M., Komro, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes AL Genome Res. 10 (10), 1617-1630 (2000)
RESULT 1 AK052901 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNEL MEDLINE PUBMED	AUTHORS TITLE JOURNAL MEDLINE

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74 69 134 129 194 189

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CVYLVVFVPGLIGNSLVLIIIIFYQKLRTLTDVFLLNLPLADLÄFVCTLPFWAYAGTY
EWVFGTVMCKTLRGMYTMNFYVSMLTLTCITVDRFIVVVQATKAFNRQAKWKIWGQVI
CLLIWTVSLLJVSLPQIIYANDDIDKLICQYHSBEIGTMVLVIQMTLGFFLPLLTMIL
YSGIIKTLLHARNPQKHKSLKIIFLVVAVFLLTQTPFNLAMLIQSTSWEYYTITSFK
YAIVVTBATAYFRAGUK
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  (MGD|MGI:1934582, GB|NM_030712, evidence: BLASTN, 99%,
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Asnagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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/db_xref="CSTBL/67"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_sreage="16 days neonate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA library was prepared and sequenced in Mouse Genome broyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKBN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                               The RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                                                                                                       FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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URL:http://genome.gec.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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BY746127 RIKEN full-length enriched, 2 days neonate thymus thymic cells (NOD) Mus musculus cDNA clone E430004020 5', mRNA sequence.

DEFINITION

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WRL.http://genome.gsc.riken.go.jp,

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Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

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sequencing pipeline with althicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
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                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 991)
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Mus musculus
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5
                  prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
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Division of Experimental Animal Research in Riken contributed to
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/clone="E430004020"
/tissue type="thymic cells"
/cell_type="thymic cells"
/clone_lib="RiKEN full-length enriched, 2 days neonate thymus_thymic cells (NOD)"
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                                                                                          assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp)
further details.
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/strain="NOD"
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09	BESULT 6 BY746487 LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS PY746487 RIKEN full-length enriched, 2 days neonate thymus thymic cells (MDD) Mus musculus CDNA clone E430014H02 5, mRNA sequence. ACCESSION BY746487 RYMARDS SYGRAM: I GI:21714192 RYMARDS SURVEY Mus musculus (HOUSE mouse) Mus musculus (ROUSE MOUSE) Mus musculus (ROUSE MOUSE) RYMARDS SURVEY RAMMAIA: BUTHAR ROGARIA; Schurograth; Muridae, Murinae, Mus. RYMARDS RYMARDS RYMARDS RYMARDS SURVEY RYMARDS
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan. (ORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tamenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.J., Adams,M.D. and Cargill,M. Inferring noneutral evolution from human-chimp-mouse orthologous gene trios NNGE Graffill,M. Science 302 (5652), 1960-1963 (2003) NNGE Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Adams,M.D. and Cargill,M. Retriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Adams,M.D. and Cargill,M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville,MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment. Location/Qualifiers 1. 1029 // Organism="Pan troglodytes" // Mol type="genomic DNA" // Ab xref="taxon:9598" // Borne="CXCR6" // Jocus_tag="HAM0176"	Deery Match Best Local Similarity Bo.8%; Pred. No. 2: 9e-189; Batt Local Similarity Bo.8%; Pred. No. 2: 9e-189; 141 TTCAACAATTCCAGGGACCAGGAGAACGCTTCCTAACTTCAACGTTCAACGGAG 142 TTCAACAAGTTCAATGCACCAGGAGACACCTTCCTAACTTCTAACATTCAACGGAG 143 TTCAACAAGTTCAATGCACCAGGAGACACCAGGACTTCCTAACATTCTCACGAGGAG 144 TTCAACAAGTTCAATGCACCAGGAGACACCATCCTGAGATCAGAACTCCTG 154 GTCTTTTCGCCCTGCATGTAACCTGGTGTTTGTCTTGTGGTCTGGTGGAGACTCCTG 155 GTCTTTTTCCCCTGATGTACCTGGTGTTTTGTCTGTGGTCTGGTGGAGAACTCCTG 156 GTCTTTTTCCCCTGATGTACCTGGTGTTTTGTCTGTGGTCTGGTGGAGAACTCCTG 157 GTCTTTTCCCCTGGATGTACTTGTCTAAACTTGCAACACCTCTGAGAACTCCTG 158 AACTTCCTGATTATATAATTTTTCACAAAATTGCAAGACCTTCAACAGGATCTTCCTGGGCATTTTTTTCCTGGGCATTTTTTTT
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Mus musculus (house mouse)
Mus musculus (thouse mouse)
Mus musculus
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 663)
Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification method
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A0636C02-5 NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1+)
CDNA Library (Long 1) Mus musculus CDNA clone NIA:A0636C02
IMAGE:30751033 5', mRNA sequence.
                                                                 251 CTGGTTCTGATTATATACATTTTCTACCAGAAGCTGAGGACTCTGACAGATGTGTTTCTG
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: A0636 row: C column: 02
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/organism="Mus musculus"
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                                                         Contact: Yoshihide Hayashizaki
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URL:http://genome-gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
Adachi,J., Aizawa,K., Akhurara,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori.F.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyashida,H., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKKN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
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/cell type="thymic cells"
/clone_lib="RIKEN full-length enriched, 2 days neonate
thymus_thymic_cells (NOD)"
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/mol_type="mRNA"
/strain="NOD"
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         /lone lib="NIA Mouse Hematopoietic Stem Cell
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(Lin-/c-Kit-/Sca-1+) cDNA Library (Long 1)"
//noce="vector: pCNV-SpORT6 (Invitrogan); Site_1: Sall;
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Site_2: Not!) Mouse CDNA project by the Laboratory of
GeneTics National Institute on Aging (NAA), Intramural
Research Program, NIH (http://jogun.grc.nia.nih.gov/CDNA).
This is a long-transcript enriched CDNA library (Ref.
Genome Res. 11: 1552-1558 (2001). [PMID: 11544199]). Total
RNAS were obtained from Brs. Dennis Taub, Dan Longo
(National Institute on Aging, USA), Jonathan Keller
(National Cancer Institute, USA). Double-stranded cDNAs
were synthesized with an Oligo (dT) primer [Invitrogan
1.1 ug of total RNA, treated with T4 DNA polymerase, and
purified by tenhanol-precipitation. The cDNAs were ligated
to Lone-linker LL-Sal4, purified by phenol/chloroform, the
cDNAs were amplified by long-tange high fidelity PCR using
EX Taq polymerase (Trakara) with a primer Sal4-8. The
products were purified by phenol/chloroform and cloned into Sal1/Not! site of pCNV-SPORT6 plasmid
vector. The DNAS were digested with Sal1 and Not! enzymes
and cloned into Sal1/Not! site of pCNV-SPORT6 plasmid
vector. The DNAS were sandard chemical method. The
average insert size about 2.2 kb. The library was
constructed by Yulan Piao."
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Matches 660; Conserv
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Justice on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov Plate: A0641 row: F column: 09 Seg primer: M13 Reverse High quality sequence ston POLYA-No.
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                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
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A0641F09-5 NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1+)
CDNA Library (Long 1) Mus musculus CDNA clone NIA:A0641F09
IMAGE:30751555 5', mRNA sequence.
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Piao, Y., Ko,N.T., Lim, M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
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                                                                                                                                                                                                                                                                                                                                   ATGGGCACTACGAGGAGATTTCTGGCTCTTCAACAATTCCAGTGATAACAGCCAGGAGA
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                                                                                                                                                                                                                                            Gaps
                                                average insert size is about 2.2 kb. The library was constructed by Yulan Piao."
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                                                                                                                                                                        Query Match 51.7%; Score 647; DB 14; I Best Local Similarity 100.0%; Pred. No. 7.3e-180; Matches 647; Conservative 0; Mismatches 0;
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(National Institute on Aging, USA), Jonathan Keller (National Cancer Institute, USA). Double-stranded cDNAs were synthesized with an Oligo (dT) primer [Invitrogen: 5.76CTMGTTGTGATGGGGGGGCGCCTTTTTTTTTTTTTTTTTT	Query Match 50.1%; Score 627; DB 14; Length 627; Best Local Similarity 100.0%; Pred. No. 6e-174; Matches 627; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	THICTGGCTCTTC TAGGGGGGTCTTT AAGGAGGTCTTTT AAGGAGGTCTTTT AAGGAGGTCTTTT TCCCTGGTTCTG TCCCTGGTTCTG TCCCTGGTTCTG TCCCTGGTTCTG TCCCTGGTTCTG TCCCTGGTTCTG TCCCTGGTTCTG TCCCTGGTTCTG TCCTGCTGAACTTG TCCAGGCACCTATC TAGATGACTTC TAGATGACTTC TAGATGACTTC TAGATGACTTC TAGATGACTTC TAGATGACTTC TGCCATTTGCTTG TGCCATTCTG TGCCATTCTCTTG TGCCATTCTCTCTTG TGCCATTCTCTCTTG TGCCATTCTCTCTTG TGCCATTCTCTCTCTCTCTCTC TGCCATTCTCTCTCTCTCTC TGCCATTCTCTCTCTCTCTC TGCCATTCTCTCTCTCTCTC TGCCATTCTCTCTCTCTC TGCCATTCTCTCTCTCTCTC TGCCATTCTCTCTCTCTC TGCCATTCTCTCTCTCTC TCCCATTCTCTCTCTCTC TCCCATTCTCTCTC	A0631A05-5 NIA Mouse Hematopoietic Stem CDNA Library (Long 1) Mus musculus cDNA
	Qy 712 CATTGCTCACTATGATTCTGTGCTACTCAGG 742	DEBULY 10 CEP11103 A0610008-5 NIA MOUSE Hematopoietic Stem Cell (Lin-C-Kit-/Sca-1+) CONTA Library (Long 1) Mus musculus CDNA clone NIA:A0610008 ACCESSION CEP1103 TAMAS: 20748555 5', MANA sequence. ACCESSION CEP1103 CEP110	Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Drs. Dennis Taub, Dan Longo

471 360 420

651 540 600

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CA574451 innear EST 19-NOV-2002 KOG16E05-5N NIA Mouse Hematopoletic Stem Cell (Lin-/C-Kit-/Sca-1+) cDNA Library (Long) Mus musculus cDNA clone NIA:KOG16E05 Linage:30070324 5', mRNA sequence.
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Was musculus (house mouse).

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musna.

I (bases 1 to 619)

Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G.,

Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.

Systematic Analyses of N.A Mouse Hematopoietic Stem Cell

(Lin., C. Kit., Sca., 1+) cDNA Library (Long)
      61 ACAAACGCTTCCTAAAGTTCAAGGAGGTCTTTTTGCCCCTGTGTGTACCTGGTAGTGTTTG 120
                                                                                                                                                                                                                                                                                                                                                        241 CTCTGCCCTTTTGGGCCCTATGCAGGCACCTATGAGTGGGTCTTTGGCACAGTCATGTGCA 300
                                                             TCTTTGGACTGCTAGGAACTCCCTGGTTCTGATTATATACATTTTCTACCAGAAGCTGA
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                                                                                                                                                                                   GGACTCTGACAGATGTTTTCTGCTGAACTTGCCCCTGGCTGACCTGGTGTTTGTCTGTA
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Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Sulte 4000, Baltimore, MD 21224-6820, USA
Email: cdna@laur.grc.nia.nih.gov
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/mol_type="mRNA"
/strain="C57BL/6NCr"
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/dowstage="Mage="Nate: 10090"
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
Email: cdna@lgsun.grc.nia.nih.gov
Plate: A0631 row: A column: 05
Seq primer: M13 Reverse
High quality sequence stop: 628
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/db_xref="taxon:10090"
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/organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6NCr"
IMAGE:30750532 5', mRNA sequence.
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Mus musculus
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CF912382.1 GI:38183586
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Contact: Yoshihide Hayashizaki
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(Lin-/c-Kit-/Sca-1+)"
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db xref="niaEST:K0616E05-5N"
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URL:http://genome.gsc.riken.go.jp,
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suebhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9216
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481 CTTTGCCACAGATCATCTATGGCCATGTTCAAGATATTGACAAGCTTATCTGTCAGTACC
                                                                                                                                                                             541 ACAGTGAGGAGATATCCACTATGGTTCTTGTTATACAGATGACTCTGGGGGTTCTTCCTGC
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RESULT 14 CF910757

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In the constructed by Yulan Piao." CF910757 Innear EST 05-NOV-2003 MRNA linear EST 05-NOV-2003 MS064D11-5 NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1+) CDNA Library (Long 1) Mus musculus CDNA clone NIA:A0604D11 INAGE:30747982 5', mRNA sequence. 1 (bases 1 to 610) 1 Jacoy'. Ko,N'T., lim,M.K. and Ko,M.S.H.

Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification ö 198 Mus musculus (house mouse) Mus musculus Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 9 1 TCTTCAACAATTCCAGTGATAACAGCCAGGAGAACAACACTCCTAAAGTTCAAGGAGG 139 TCTTCAACAATTCCAGTGATAACAGCCAGGAGAACAAACGCTTCCTAAAGTTCAAGGAGG Gaps Contact: Dawcod B. Dudekula Laboratory of Genetics National Institute on Aging/National Institutes of Health National Institute on Aging/National Institutes of Health Basic chae@lgsun.grc.nia.nih.gov Plate: A0604 row: D column: 11 Seg primer: M13 Reverse High quality sequence stop: 610 ; Length 610; Query Match
48.8%; Score 610; DB 14; Length 6
Best Local Similarity 100.0%; Pred. No. 6.4e-169;
Matches 610; Conservative 0; Mismatches 0; Indels Genome Res. 11 (9), 1553-1558 (2001) Location/Qualifiers CF910757.1 GI:38181933 ð d

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/db.xte="knash.10090"

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Best Local Similarity 99.8%; Pred. No. 8.7e-166;
Matches 600; Conservative 0; Mismatches 1; Indels 0;
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/db_xref="taxon:10090"
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٥'n	679 TIGITATACAGATGACTCIGGGGTICTTCCTGCCATTGCTCACTATGATTCTGTGCTACT 738
qa	541 TICTIAIACAGATGACTCTGGGGTTCTTCCTGCCATTGCTCACTATGATTCTGTGCTACT 600
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QQ	601 C 601
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APPLICANY: Blahourbagy, Nabil A.
APPLICANY: Blahourbagy, Nabil A.
APPLICANY: Blahourbagy, Nabil A.
APPLICANY: Blis, Catherine E.
TITLE OF INVENTION: Human 7-Transmembrane Receptor
NUMBER OF SOUTHORS: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STRET: 709 Swedland Road
CITY: King of Prussia
STATE: Pennsylvania
COWNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,011
FILING DATE:
FILING DATE:
FILING DATE:
FREFERNCE/DOCKET NUMBER: 34,344
REFERENCE/DOCKET NUMBER: 310-270-5219
TELEPACH FOR SOUTH STATES SOUTH STELEPHONE: 610-270-5090
INPORMATION FOR SERQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FUNCTH: 22348 base bairs
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Pred. No. 6.3e-224;
0; Mismatches 231;
US-09-299-843A-6
US-09-08-337B-6
PCT-US93-11153-6
US-08-153-848-14
US-09-088-337B-14
US-09-083-337B-14
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US-08-450-393A-3
US-08-446-669-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1, Application US/08742011; Patent No. 5824504; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 78.6%;
Matches 871; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
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   TOPOLOGY: 11 MOLECULE TYPE:
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US-08-742-011-1
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Sequence 1, Appli
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Sequence 1, Appli
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US-09-106-434-1095

US-09-08-3378-23

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Ramani, Vineet N.K.

TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS

ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF

IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OFFRANTS: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/116,498

FILING DATE: 16-Jul-1998

CLASSIFICATION: CURKNOWN>

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET WINDER: 1049-1-009

TELEPHONE: 201-487-5800

TELEPHONE: 201-343-1684

INFORMATION FOR REQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1029 base pairs

TTYPE: nucleic acid

STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David N. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1442 TTATAGCTTGCGCATTCTCATGGAGAAG 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: pigtail macaque SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                     Sequence 5, Application US/09116498 Patent No. 6251582 GENERAL INFORMATION:
                                                                                                                                                                      APPLICANT: Littman, Dan I
Deng, Hongkui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                               Floor
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Matches 811; Conserv
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                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,498
FILING DATE: IG-Jul-1998
CLASSIFICATION: CURRENT APPLICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 685; DB 3; L
Pred. No. 4.8e-217;
O; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                    NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009
TELECOMMUNICATION INFORMATION:
TELEPAX: 201-487-5800
TELEPAX: 201-487-5800
INFORMATION FOR SGO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1037 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: African Green Monkey
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
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Best Local Similarity 81.1%;
Matches 809; Conservative
                                                                                  COMPUTER READABLE FORM:
STATE: New Jersey
                            USA
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Unutmaz, Derya
Ramani, Vineet N.K.
INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
THEREOF
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ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
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; Sequence 3, Application US/09116498
; Patent No. 6251582
; GENERAL INFORMATION:
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| Patent No. 6232084
| GENERAL INFORMATION:
| APPLICANT: MACPHER, COLIN HOUSTON
| APPLICANT: MACPHER, COLIN HOUSTON
| TITLE OF INVENTION: NEW USE
| FILE REPRENCES: GH=31106
| CURRENT PELING DATE: 1999-03-24
| PRIOR APPLICATION NUMBER: 9806677.2
| PRIOR APPLICATION NUMBER: 9806677.2
| PRIOR APPLICATION NUMBER: 9806677.2
| PRIOR FILING DATE: 1998-03-27
| NUMBER OF SEQ ID NOS: 9
| SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-275-384B-4
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APPLICANT: Murphy, Kristine E. APPLICANT: Wilbanks, Alyson M. APPLICANT: Wilbanks, Alyson M. TITLE OF INVENTION: Chemokine Receptor TITLE OF INVENTION: Chemokine Receptor; TITLE OF INVENTION: US/09/449,437A; CURRENT APPLICATION NUMBER: US/09/449,437A; CURRENT FILING DATE: 2001-01-09; NUMBER: OF SEQ ID NOS: 18; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 1. LENGTH: 1029
                                                                                                                                            GATCATCTTCCTTGTAGTGGCTGTGTTCCTGCTGACCCCAGACACCCTTGCCAT
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Pred. No. 4.1e-215;
0; Mismatches 182;
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Best Local Similarity 81.2%;
Matches 786; Conservative (
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ORGANISM: Homo sapiens
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,498
FILING DATE: 16-Jul-1998
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
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STRANDEDNESS: double
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80.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Hackensack
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Best Local Similarity
                                                     RESULT 6
US-09-116-498-1
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Pred. No. 2.5e-214;
); Mismatches 181;
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81.2%;
                                               Query Match
Best Local Similarity 81.2
Matches 783; Conservative
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Sequence 1, Application US/09116498
Patent No. 6251582
GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
Dang, Hongkui
Unutmaz, Derya
Ramani, Vineet N.K.
TITLE OF INVENTION: NOVELA LITTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL BYTRY INTO CELLS, METHODS OF IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
COPTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 185;
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Pred. No. 9.4e-205;
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1719 ACCEMENDACINGGENERAL MACCINATION CONTINUED CONTINUE	Query Match 14.7%; Score 183.4; DB 4; Length 1074; Best Local Similarity 52.9%; Pred. No. 2.3e-50; Matches 490; Conservative 0; Mismatches 401; Indels 36; Gaps 14.7%; Pred. No. 2.3e-50; Matches 490; Conservative 0; Mismatches 401; Indels 36; Gaps 14.7%; Pred. No. 2.3e-50; Matches 400; Conservative 0; Mismatches 401; Indels 36; Gaps	CAACTICACTGACTICTACTGTGAGAAAACAATGTCAGGCAGTTTGCGAGCCATTTCCT 11 GCCCTGTGTGTACCTGGTAGTGTTTGTCTTTGGACTGCTAGGAAACTCCCTGGTTCTGAT 26	177 †GTCTACTGGTACTGCACAAGAGTGAAGACCATGACCGACATGTTCCTTTTGAATTTGGC 2 326 CCTGGCTGACCTGGTGTTTGTCTGTCCTCTTTTGGCCTATGGAGCACCTATGG 237 AATTGCTGACCTCTTTCTTGTCACTCTTCCCTTCTGGGCCATTGCTGCTGCTGACCA 2 386 GTGGGTCTTTGGCACAGTCATGTCACATTCGAGCATGCTACAGAACTTCTA 4	297 44 6 3357 506	417 CAIGAGAGCACATACTIGGAGGAGAAAAGGCTTTTGTACGAAAATGGTTTGCTTAAG 566 CAITTGGGTGTCTCCTGTTGGTTTCTTTGCCACAGATCATCTATGGCCATGTTCAAGA 11	w		OY 848 CCTTGCCATGTTAATCCAAAGTACAAGGTTATACCATAACCAGCTTAAGTA 907 Db 777 CTGCATGTTAATCCAAAGTACAAGGTTACTATCCAACTGTGCGT 836 OY 908 TGCCATCGTAGGTGAAGGCTATAGCATATCTTCCAACTGTGCGT 849 Db 837 TTCCACCAACATTGACATCTGCTTCCAGACGAACACTCTCTCCAAGTTG 896 OY 950 CCTTAACCCTGTACTTTTTTGTTGCTTTGTTAAGTTCCGAAAACTTCAAGTTG 896 OY 950 CCTTAACCCTGTACTTTTTTTTTTTTTTTTTTTTTTTTT
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CCTTAACCCTGTACTTTATGCCTTTGTTGGCTTAAAGTTCCGGAAGAACGTCTGGAAACT 1009
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        CIGCAITTIGITGETGCACCATTGACGCCTATGCCATGTTCATCTCCAACTGTGCCGT 893
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                                                                                                                                   ------TCGTAGTGACAGAGGCTATAGCATACTTTCGGGCTTG
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Fatent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESSES: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STREET: ALLO ALTO
COMMENDED: COLLIFORNIA
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Pred. No. 4.1e-50;
0; Mismatches 401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                1010 TATGAAGGATATCGGCTGCCTCTCTCA 1036
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TELECOMONICATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1095:
SEGURENCE CHARACTERISTICS:
LENGTH: 2577 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 52.9%;
Matches 490; Conservative
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE: GENBANK

CLONE: 91245054

US-09-016-434-1095
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                                                                                                                               908 TGCCA
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                     APPLICANT: Andrew, David P.
APPLICANT: Andrew, Parian A.
APPLICANT: Sabel, Brian A.
APPLICANT: Shoul D.
TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
TITLE OF INVENTION: IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION
FILE REFERENCE: LKS99-10 10 DENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION
CURRENT APPLICATION NUMBER: US/09/266,464
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PastERQ for Windows Version 3.0

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             CITY:
Chicago
STATE: 111nois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
14.5%; Score 181.2; DB 1;
Best Local Similarity 53.2%; Pred. No. 2.3e-49;
Matches 481; Conservative 0; Mismatches 383;
                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 57598048nd, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-630
TELEFAX: (312) 474-648
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2751 base pairs
TYPE: NUCLEIC SINGLE
TYPE: NUCLEIC SINGLE
TYPE: NUCLEIC SINGLE
TYPE: NUCLEIC SINGLE
TYPE: NUCLEIC SINGLE
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TYPE: NUCLEIC SINGLE
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FEATURE:
NAME/KEY: intron
LOCATION: 1..691
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2341..2348
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692..1768
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LOCATION:
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LOCATION:
US-08-153-848-23
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| Patent No. 5758004
| GENERAL INFORMATION:
| APPLICANT: Godiska, Ronald
| APPLICANT: Gray, Patrick W. |
| APPLICANT: Schweikart, Vicki L. |
| TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors NUMBER OF SEQUENCES: 64 |
| CORRESPONDENCE ADDRESS: ADDRESSE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
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US-08-153-848-23
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Pred. No. 2.3e-49;
0; Mismatches 383;
                                                                                                                                              NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION:
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6300
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 53.2%;
Matches 481; Conservative
                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 2751 Base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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2341..2348
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Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
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STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: 111inois
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
                                                                                                                         TCTTTGCCACAGATCATCTATGGCCATGTTCAAGATA
                       AAGTGGAAGATCTGGGGCCAAGTCATTTGCTTGCTCA
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PALOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-UNN-1998
PRIOR APPLICATION DATA:
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
TYPE: nucleic acid
STRANDEDNESS: single
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Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
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CITY: Chicago
STATE: Illinois
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: «Unknown»
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
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APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
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Patent No. 6348574
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
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TELEFAX: (312) 474-0448
TELEX: 25-3856
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SEQUENCE CHARACTERISTICS:
LENGTH: 2751 base pairs
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COMPUTER READABLE FORM:
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14.5%; Score 181.2; DB 4;
Best Local Similarity 53.2%; Pred. No. 2.3e-49;
Matches 481; Conservative 0; Mismatches 383;
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, NAME/KEY: polyA_signal
; LOCATION: 2341...2348
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-088-337B-23
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Length 2751;
                                                                 Indels
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Score 181.2; DB 5;
Pred. No. 2.3e-49;
0; Mismatches 383;
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2.09-170-496D-175
; Sequence 175, Application US/09170496D
; Patent No. 6555339
14.5%;
                                Best Local Similarity 53.2
Matches 481; Conservative
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TTGTTGGCTTAAAGTTCCGGAAGAACGTCTGGAAACTTATGAAGGATATCGGCTGCCTCT 1032
                                                                                                                                  1557 ATGACGTCACCTACAGCCTCGGTCCGCTGCTGCTCAACCCTTTCTTGTATGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23, Application PC/TUS9311153
GENERAL INFORMATION.
BAPFLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikarr, Vicki L.
TILLE OPT INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
                                                             913 TCGTAGTGACAGGCTATAGCATACTTTCGGGCTTGCCTTAACCC
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6300 Sears Tower, 233 South Wacker Drive
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ADDRESSEE: Marchall, O'Toole, Gerstein, Murray
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRANT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
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APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
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ER: 31794
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REPERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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nucleic acid
DNESS: single
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692..1768
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CITY: Chicago
STATE: Illinois
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STRANDEDNESS:
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PCT-US93-11153-23
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NAME/KEY:
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NAME/KEY:
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FEATURE:
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NAME/KEY:
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TCGTAGTGACAGAGCTATAGCATACTTTCGGGCTTG
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Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
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PatentIn Release #1.0, Version #1.25
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14.2%; Score 177.8; DB 3;
Best Local Similarity 52.9%; Pred. No. 2.6e-48;
Matches 477; Conservative 0; Mismatches 387;
                                                                                                                                                                                                                                                                                                                           1010 TATGAAGGATATCGGCTGCCTCTCTCA 1036
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REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION 174-6300
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                   957 CCTGAAGAACTIGGGTIGCATCAGCCA 983
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-UN-1998
PRIOR APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
FILING DATE: 17-NOV-1993
PRIOR APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1993
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
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177..1310
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STRANDEDNESS: sing
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SOFTWARE: Patenti
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
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US-09-299-843A-65
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US-09-299-843A-65
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                                  APPLICANT: Behan, Dominic P.
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G 1
TITLE OF INVENTION: Receptors
FILE REPERBURCE: AREN 0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT APPLICATION NUMBER: US/09/170,496D
SURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFFWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 178.6; DB 4; Length
Pred. No. 8.9e-49;
0; Mismatches 404; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 52.5%;
Matches 487; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-175
    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1074
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Search completed: September 29, 2004, 03:02:04 Job time : 125 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LCCATION: 2008
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13566
                                      TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
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                                                                                                                                                         5; Search time 637 Seconds (without alignments) 9947.020 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
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| cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
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| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
                 GenCore version 5.1.6
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13 US-10-342-896-1259
13 US-10-372-189-1299
13 US-10-225-567A-347
13 US-10-225-567A-347
13 US-09-852-156-5
9 US-09-852-156-3
15 US-10-083-168-3
9 US-09-940-063-1
9 US-10-174-293-1
9 US-10-174-293-1
9 US-10-083-168-64
6 9 US-09-852-156-1
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Maximum Match 100%
Listing first 45 summaries
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175, App
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APPLICANT: Mangy Youzhon
APPLICANT: Way Yougyao
APPLICANT: Wangy Youzhon
APPLICANT: Wangy Youzhon
APPLICANT: Wangy Youzhon
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: POR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/336,220
PRIOR PILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13566
LENGTH: 2008
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US-10-172-118-678
US-10-225-567A-67
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Best Local Similarity 78.5%;
Matches 870; Conservative 0
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US-10-342-887-1299
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Pred. No. 1.1e-224;
0; Mismatches 232; Indels 6;
Sequence 1299, Application US/10342887
Sequence 1299, Application US/10342887
Publication No. U520040058340A1
GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: Linsley, Peter S.
APPLICANT: Mao, Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Won't Veer, Laura Johanna
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Van de Vijver, Marc J.
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                          TCAGGCATTATCAAGACCTTGCTTCATGCTCGAAACTTCCAGAAGCACAAATCTCTAAAG 797
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NM_006564
DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1299
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Sequence 1, Application US/10458110

Sequence 1, Application US/10458110

Sequence 1, Application No. US20030203450A1

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as represented APPLICANT: Dy the Secretary, Department of Health and Human Services APPLICANT: Falsi Liao

APPLICANT: Ghalib Alkhatib

APPLICANT: Ghalib Alkhatib

APPLICANT: Ghalib Alkhatib

APPLICANT: Ghalib Alkhatib

APPLICANT: MITH HUMAN HUV INFECTION

FILE REPERBUCE: 14014.033

CURRENT APPLICATION NUMBER: US/10/458,110

CURRENT FILING DATE: 1999-12-22

PRIOR APPLICATION NUMBER: US 60/042,275

PRIOR PELICATION NUMBER: US 60/042,880

FRICH RELING DATE: 1999-03-31

PRIOR APPLICATION NUMBER: US 60/042,880

FRICH APPLICATION NUMBER: US 60/042,880

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Matches 870; Conservative
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; LOCATION: (31)...(1056)
US-10-458-110-1
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                                                                                                                                                                                        APPLICANT: Lifeban Biosciences
APPLICANT: Exemple Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: 06/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR PILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 347
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                                                                                                                    Sequence 347, Application US/10225567A Publication No. US20030113798A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 78.5'
Matches 870; Conservative
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ORGANISM: Homo sapiens
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Deng, Hongkui
Unutmaz, Derya
Ramani, Vineet N.K.
INVENTION: NOEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 CCTTTTGGGCCTATGCAGGCACCTATGAGTGGGTCTTTGGCACAGTCATGTGCAAAAACTC 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: David A. Jackson, Esq. STREET: 411 Hackensack Ave, Continental Plaza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version
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Pred. No. 1.7e-219;
0; Mismatches 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009NCIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER REDABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: Patentln Release #1.0, Ver
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/09/852,156
FILING DATE: 09-May-2001
CLASSIFICATION: <Unknown>
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1029 base pairs
TYPE: noleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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ilarity 79.8%;
Conservative C
RESULT 6
US-09-852-156-5
Sequence 5, Application US/098:
Fatent No. US20020076694A1
GENERAL INFORMATION:
APPLICANT: Littman, Da
THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO THOMGO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A
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COUNTRY: USA
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Matches 811;
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                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/852,156
FILING DATE: 09-May-2001
CLASSIFICATION: <UNknown>
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54.8%; Score 685; DB 9; L
Best Local Similarity 81.1%; Pred. No. 5e-218;
Matches 809; Conservative 0; Mismatches 185;
                                                                                                                                                                                      NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009NCIP
TELECOMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: African Green Monkey
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1037 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
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Ramani, Vineet N.K.
Ramani, Vineet M.K.
INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
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CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09852156
Patent No. US20020076694A1
GENERAL INFORMATION:
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STATE: New Jersey
COUNTRY: USA
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APPLICANT: Briskin, Michael J.
APPLICANT: Briskin, Michael J.
APPLICANT: Briskin, Michael J.
APPLICANT: Murphy, Kristine E.
APPLICANT: Wilbanks, Alyson M.
APPLICANT: Wilbanks, Alyson M.
TITLE OF INVENTION: One-control Receptor
FILE REPERENCE: 1855.1070-000
CURRENT APPLICATION NUMBER: US/09/940,063
PRIOR APPLICATION NUMBER: 09/449,437
PRIOR PLINIO DATE: 2001-08-27
PRIOR PLINIO DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                         TGTGCAAAACTCTTCGAGGCATGTATACAATGAACTTCTACGTGTCCATGCTCACTCTCA
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US-10-083-168-3

US-10-083-168-3

SQUENCE 3, Application US/10083168

Publication No. US20030023069A1

GENERAL INFORMATION:

APPLICANT: Chalmers, Derek T.

APPLICANT: Behan, Dominic P.

APPLICANT: Behan, Dominic P.

APPLICANT: Dominic P.

APPLICANT: Lin, I-Lin

APPLICANT: Lin, I-Lin

TITLE OF INVENTION: Receptors

FILE REPREENCE: Langerous And No. US20030023069A1-Endogenous, Constitutively Act

TITLE OF INVENTION: Receptors

FILE PREFENCE: APPLICANT: US/10/083,168

CURRENT APPLICATION NUMBER: US/10/083,168

CURRENT FILING DATE: 2002-02-26

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH: 1029
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                                                                                                     GATCATCTTCCTTGTAGTGGCTGTGTTCCTGCTGACCCAGACACCCTTCAACCTTGCCAT 856
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CORGANISM: Homo sapiens
US-10-083-168-3
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APPLICANT: Murphy, Kristine E.
APPLICANT: Wilbanks, Alyson M.
APPLICANT: Wilbanks, Alyson M.
APPLICANT: Wilbanks, Alyson M.
APPLICANT: Wilbanks, Alyson M.
APPLICANT: Wilbanks, Alyson M.
APPLICANT: Wilbanks, Alyson M.
TITLE OF INVENTION: No. US20030165995Alel Antibodies and Ligands for TITLE OF INVENTION: Chemokine Receptor
FILE REPRENCE: 1855.1070-001.
FILE OF INVENTION: Chemokine Receptor
FILE OF INVENTION NUMBER: US/10/174,293
CURRENT APPLICATION NUMBER: US/09/722,064
PRIOR APPLICATION NUMBER: US 09/449,437
PRIOR PILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 27
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81.2%; Pred. No. 4.4e-216;
live 0; Mismatches 182; Indels 0;
                                                                                                                                                                       Sequence 1, Application US/10174293 Publication No. US20030165995A1 GENERAL INFORMATION:
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Best Local Similarity 81.2'
Matches 786; Conservative
                         1133
                                                                 1022 AGTTATAG 1029
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US-10-174-293-1
                       1126 AATTGTAG
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Pred. No. 4.4e-216;
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Best Local Similarity 81.2%;
Matches 786; Conservative
; SEQ ID NO 1
; LENGTH: 1029
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-940-063-1
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Pred. No. 4.4e-216;
0; Mismatches 182; Indels
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PRIOR FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: 60/404,904
PRIOR FILING DATE: 2002-08-21
PRIOR PLING DATE: 2002-08-23
PRIOR PLING DATE: 2002-08-23
REGRAINING PRIOR APPLICATION NUMBER: 60/405,450
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FastSEQ for Windows Version 4.0
SERGITH: 1029
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Best Local Similarity 81.2%;
Matches 786; Conservative
                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo Sapiens
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GENERAL INCORMATION

APPLICANT: Chun, Miyoung

APPLICANT: Chun, Miyoung

APPLICANT: Cally, Allen

APPLICANT: Cally, Allen

APPLICANT: Acton, Susan L.

APPLICANT: Acton, Susan L.

APPLICANT: Stagliano, Name,

APPLICANT: Stagliano, Name,

APPLICANT: Stagliano, Name,

APPLICANT: Stagliano, Name,

APPLICANT: Stagliano, Name,

APPLICANT: Stagliano, Name,

APPLICANT: Applicant: Acton, 3202, 4143, 18036, 16105, 38650,

TITLE OF INVENTION: CANTAGONASCULAR GISCASCULAR G
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Sequence 5, Application US/10353690 Publication No. US20030215840A1 GENERAL INFORMATION:
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APPLICANT: Littman, Dan R.
Deng, Hongkui
Unutenaz, Derya
Ramani, Vineet N.K.
TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
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                                                                                                           <u> AGTACCACAGTGAGGAGATATCCACTATGGTTCTTGTTATACAGATGACTCTGGGGGTTCT</u>
                                                                                                                                                GTTACCATGACGAGGGAATTTCCACTGTGGTTCTTGCCACCCAGATGACACTGGGGTTCT
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CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/852,156
FILING DATE: 09-May-2001
CLASSIFICATION: <UNKnown>
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Patent No. US20020076694A1
GENERAL INFORMATION:
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COUNTRY: USA
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APPLICANT: Cottuno, Daniel
APPLICANT: Cottuno, Daniel
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Endogenous And No. US20030023069Al-Endogenous, Constitutively Act
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0320
CURRENT PELLING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.1
SEQ ID NO 64
LENGTH: 1029
                                                                                                                                  CTGAGGACAGTTCCAAGACTTGTTCTGCCTCCCACAATGTAGAGACCACCAGTATGTTCC 1125
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                            AACTTATGAAGGATATCGGCTGCCTCTCTCACCTGGGAGTCTCAAGTCAATGGAAGTCTT 1065
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81.0%; Pred. No. 5.2e-215;
iive 0; Mismatches 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 64, Application US/10083168
Publication No. US20030023069A1
GENERAL INFORMATION:
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APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Dominic P.
APPLICANT: Maciejewski-Lenior,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 81.0
Matches 784; Conservative
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ORGANISM: Unknown
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/ Sequence 23, Application US/10251385
// Sequence 23, Application US/10251385
// Publication No. US2003105292A1
// GENERAL INFORMATION:
// APPLICANT: Behan, Dominic P.
// APPLICANT: Liaw, Chen W.
// TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
// TITLE OF INVENTION: Receptors
// TITLE OF INVENTION: Receptors
// TITLE OF INVENTION: Receptors
// TITLE OF INVENTION: Receptors
// TITLE OF INVENTION: Receptors
// TITLE OF INVENTION: USPERS: US/09/10/251,385
// CURRENT FILING DATE: 1998-110-13
// WUMBER OF SEQ ID NOS: 294
// SOFTWARR: PatentIn version 3.1
// SOFTWARR: PatentIn version 3.1
// SOFTWARR: COA3.
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                                                                        811 GTGACAGAGGCCATCGCATACCTGAGGGCCTGCCTTAAACCCTGTGCTCTATGCCTTTGTC 870
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 490; Conserv
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US-10-251-385-23
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US-10-251-385-23
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Best Local Similarity 80.8%; Pred. No. 1.3e-205;
Matches 805; Conservative 0; Mismatches 185; Indels
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009NCIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-43-1644
INFORMATION FOR SEQ ID No: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: CDATE TYPE: CDA
HYPOTHET TYPE: CDA
HYPOTHET TYPE: CDA
HYPOTHET SOURCE:
                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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